



results of BLAST

BLASTN 2.2.11 [Jun-05-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1124291504-12319-167553306596.BLASTQ2

Query=

(48 letters)

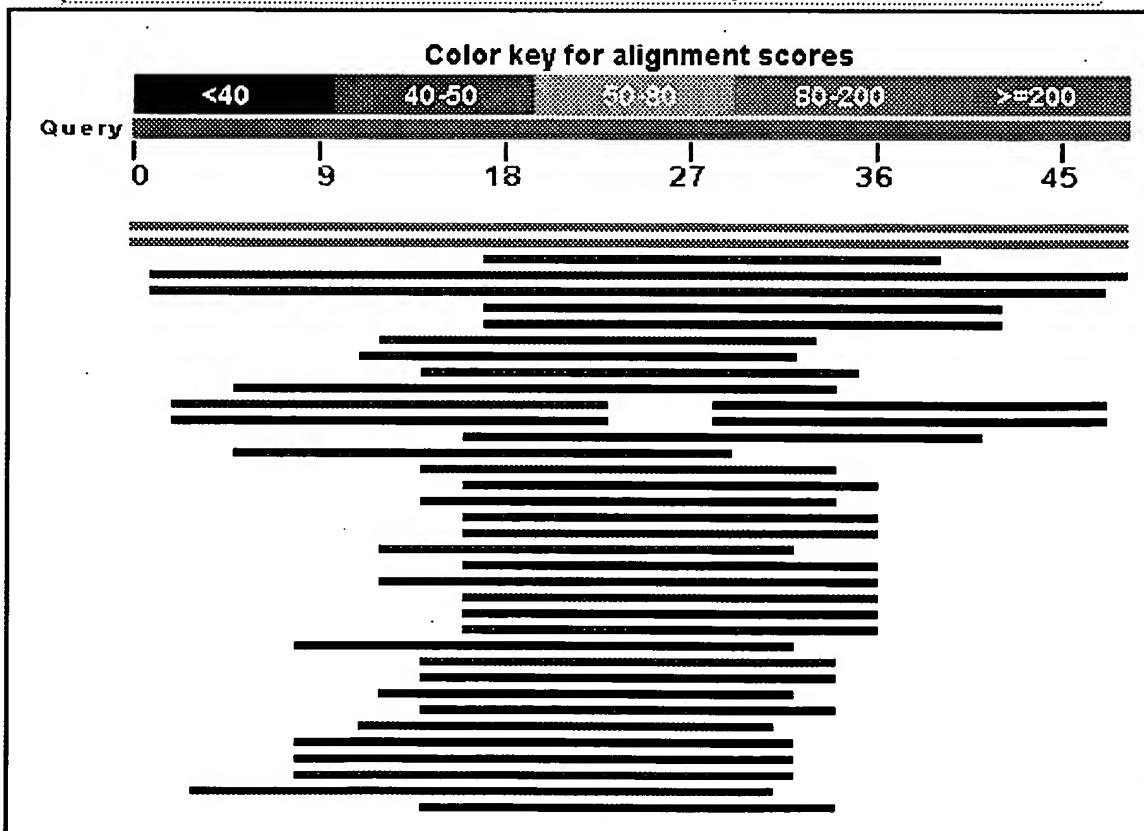
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,413,089 sequences; 14,885,149,293 total letters

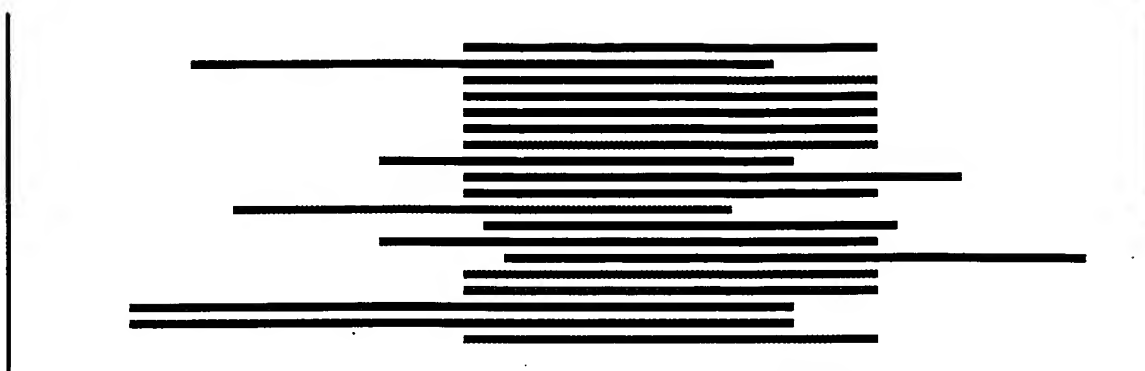
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

Distribution of 102 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments





Sequences producing significant alignments:			Score (Bits)	E Value
gi 4103165 gb AF021919.1 AF021919	Actinobacillus pleuropneumo...		95.6	7e-18
gi 4103979 gb AF030511.1 AF030511	Actinobacillus pleuropneumo...		87.7	2e-15
gi 18098529 gb AC093716.3 	Homo sapiens BAC clone RP11-702L4 fro		44.1	0.022
gi 14550318 gb AC015933.9 	Homo sapiens chromosome 18, clone CTD		44.1	0.022
gi 21281558 gb AC110015.5 	Homo sapiens chromosome 18, clone ...		44.1	0.022
gi 37060013 gb AC123876.5 	Mus musculus BAC clone RP23-270P19...		42.1	0.087
gi 34740427 gb AC125373.4 	Mus musculus BAC clone RP23-379A13...		42.1	0.087
gi 37651868 gb AC125065.3 	Mus musculus BAC clone RP23-430G6 ...		42.1	0.087
gi 25168704 emb AL845507.8 	Zebrafish DNA sequence from clone...		42.1	0.087
gi 31581035 dbj AP006404.1 	Lotus corniculatus var. japonicus...		42.1	0.087
gi 17149788 gb AC098861.2 	Homo sapiens BAC clone RP11-297J2 fro		42.1	0.087
gi 25075790 gb AC007546.6 	Homo sapiens 12 BAC RP11-946P6 (Ro...		42.1	0.087
gi 15808547 gb AC093214.2 	Homo sapiens chromosome 5 clone CTD-2		42.1	0.087
gi 15451667 gb AC016594.7 	Homo sapiens chromosome 5 clone CTD-2		42.1	0.087
gi 165657 gb J03744.1 RABPLP2	Rabbit myelin P2 mRNA, complete cd		42.1	0.087
gi 28626888 gb AC129302.3 	Mus musculus BAC clone RP24-441C24...		40.1	0.34
gi 38044253 gb AC102368.6 	Mus musculus chromosome 14, clone RP2		40.1	0.34
gi 15012100 gb BC010956.1 	Homo sapiens fibroblast growth fac...		40.1	0.34
gi 33235829 gb AC145772.1 	Pan troglodytes BAC clone RP43-14J20		40.1	0.34
gi 46518131 emb BX248323.8 	Zebrafish DNA sequence from clone...		40.1	0.34
gi 32402490 gb AY331807.1 	Homo sapiens N-acetyltransferase 2...		40.1	0.34
gi 4557782 ref NM_000015.1 	Homo sapiens N-acetyltransferase ...		40.1	0.34
gi 70921875 ref XM_729101.1 	hypothetical protein (PC105701.00.0		40.1	0.34
gi 55630291 ref XM_519631.1 	PREDICTED: Pan troglodytes simil...		40.1	0.34
gi 70887900 gb AC151286.3 	Mus musculus BAC clone RP23-368B8 ...		40.1	0.34
gi 28227 emb X14672.1 HSAACT	Human gene for arylamine N-acetyltr		40.1	0.34
gi 7630158 emb AL353012.1 SPBC1711	S.pombe chromosome II cosmid		40.1	0.34
gi 24211331 gb AC120051.5 	Homo sapiens chromosome 8, clone RP11		40.1	0.34
gi 41582918 gb AE017202.1 	Lactobacillus johnsonii NCC 533, s...		40.1	0.34
gi 39752574 emb BX664601.6 	Zebrafish DNA sequence from clone...		40.1	0.34
gi 38323074 emb BX465190.4 	Zebrafish DNA sequence from clone...		40.1	0.34
gi 28829570 gb AC117176.2 	Dictyostelium discoideum chromosom...		40.1	0.34
gi 58696608 emb CR356236.12 	Zebrafish DNA sequence from clon...		40.1	0.34
gi 41352298 gb AY531391.1 	Schizaphis graminum mitochondrion, co		40.1	0.34
gi 27923645 gb AC137810.3 	Homo sapiens chromosome 5 clone XXfos		40.1	0.34
gi 20198523 gb AC116333.2 	Homo sapiens chromosome 5 clone CTD-2		40.1	0.34
gi 20197301 gb AC005171.3 	Arabidopsis thaliana chromosome 2 ...		40.1	0.34
gi 19747134 gb AC074132.5 	Homo sapiens chromosome 5 clone CTD-2		40.1	0.34
gi 19071579 gb AC025919.8 	Homo sapiens chromosome 15 clone R...		40.1	0.34
gi 15809172 gb AC093831.3 	Homo sapiens BAC clone RP11-401I19 fr		40.1	0.34

gi 18921296 qb AC093281.2 	Homo sapiens chromosome 5 clone RP11-	40.1	0.34	
gi 18056697 qb AC025062.6 	Homo sapiens chromosome 8, clone RP11	40.1	0.34	
gi 45501306 qb BC067218.1 	Homo sapiens N-acetyltransferase 2...	40.1	0.34	
gi 6457296 qb AF179626.1 AF179626	Expression vector pGP100, comp	40.1	0.34	
gi 219415 dbj D90042.1 HUMAACTA3	Homo sapiens mRNA for arylam...	40.1	0.34	
gi 219411 dbj D90040.1 HUMAACTA1	Homo sapiens mRNA for arylam...	40.1	0.34	
gi 46879303 qb AC091332.8 	Mus musculus chromosome 17, clone RP2	40.1	0.34	
gi 46309633 qb AC123880.18 	Mus musculus chromosome 3, clone RP2	40.1	0.34	
gi 2731603 qb AC003960.1 AC003960	Human Cosmid g5129g129 from 7q	40.1	0.34	
gi 24430263 emb AL928739.5 	Mouse DNA sequence from clone RP2...	40.1	0.34	
gi 23304094 emb AL672031.9 	Mouse DNA sequence from clone RP2...	40.1	0.34	
gi 26092098 dbj AK047329.1 	Mus musculus 10 days neonate cere...	40.1	0.34	
gi 15431246 qb AC068042.5 	Homo sapiens BAC clone RP11-535B12 fr	40.1	0.34	
gi 62460846 qb AC154717.2 	Mus musculus BAC clone RP24-369E16...	40.1	0.34	
gi 62123187 qb AC154187.2 	Mus musculus BAC clone RP24-444N2 ...	40.1	0.34	
gi 5059233 qb AF147845.1 AF147845	Parapsilocephala sp. 28S ribos	40.1	0.34	
gi 5059231 qb AF147843.1 AF147843	Bonjeania sp. 1 28S ribosomal	40.1	0.34	
gi 219877 dbj D10872.1 HUMHNAT32	Humam h NAT allele 3-2 gene for	40.1	0.34	
gi 219874 dbj D10871.1 HUMHNAT22	Human h NAT allele 2-2 gene for	40.1	0.34	
gi 219871 dbj D10870.1 HUMHNAT12	Human h NAT allele 1-2 gene for	40.1	0.34	
gi 30522935 qb AC123841.4 	Mus musculus BAC clone RP23-400M7 ...	38.2	1.4	
gi 23499682 qb AC121568.3 	Mus musculus BAC clone RP23-226F18 fr	38.2	1.4	
gi 70935945 ref XM_733896.1 	hypothetical protein (PC000461.04.0	38.2	1.4	
gi 13443441 emb AL445584.16 	Human DNA sequence from clone RP...	38.2	1.4	
gi 56542279 emb AL162415.16 	Human DNA sequence from clone RP...	38.2	1.4	
gi 41392246 emb AL139141.23 	Human DNA sequence from clone RP...	38.2	1.4	
gi 15282137 emb AL157783.15 	Human DNA sequence from clone RP...	38.2	1.4	
gi 35209654 emb BX530036.7 	Zebrafish DNA sequence from clone...	38.2	1.4	
gi 21263329 qb AC099818.2 	Homo sapiens chromosome 8, clone RP11	38.2	1.4	
gi 14277165 qb AC073581.23 	Homo sapiens 8 BAC RP11-42902 (Ro...	38.2	1.4	
gi 56798018 emb CR925830.3 	Human DNA sequence from clone RP1...	38.2	1.4	
gi 38044013 emb BX664609.6 	Human DNA sequence from clone RP1...	38.2	1.4	
gi 51234144 qb AY714780.1 	Homo sapiens carboxypeptidase B2 (...	38.2	1.4	
gi 68467483 ref XM_717082.1 	hypothetical protein (Ca019_4965) m	38.2	1.4	
gi 68467250 ref XM_717194.1 	hypothetical protein (Ca019_12430)	38.2	1.4	
gi 56550491 emb CR339043.11 	Zebrafish DNA sequence from clon...	38.2	1.4	
gi 56541872 emb BX324201.7 	Zebrafish DNA sequence from clone...	38.2	1.4	
gi 38524391 emb BX649534.9 	Zebrafish DNA sequence from clone...	38.2	1.4	
gi 61740788 qb AC149601.3 	Medicago truncatula chromosome 7 B...	38.2	1.4	
gi 19698727 qb AC084740.5 	Homo sapiens BAC clone RP11-423E20 fr	38.2	1.4	
gi 19881533 qb AC012047.8 	Homo sapiens chromosome 10 clone RP11	38.2	1.4	
gi 19774485 qb AC116310.2 	Homo sapiens chromosome 5 clone RP11-	38.2	1.4	
gi 19774306 qb AC112918.3 	Homo sapiens X BAC RP11-370L12 (Ro...	38.2	1.4	
gi 18056717 qb AC104068.3 	Homo sapiens BAC clone RP11-252F15 fr	38.2	1.4	
gi 18482313 qb AC104791.3 	Homo sapiens BAC clone RP11-181K12 fr	38.2	1.4	
gi 48926772 qb AC133092.4 	Mus musculus BAC clone RP23-404G6 ...	38.2	1.4	
gi 68068246 ref XM_670941.1 	Plasmodium berghei conserved hyp...	38.2	1.4	
gi 68064473 ref XM_669129.1 	Plasmodium berghei hypothetical ...	38.2	1.4	
gi 18151020 qb AC092054.2 	Homo sapiens chromosome 3 clone RP11-	38.2	1.4	
gi 18042465 qb AC080082.4 	Homo sapiens BAC clone RP11-531D14 fr	38.2	1.4	
gi 67010238 qb AC154596.2 	Mus musculus BAC clone RP23-354C17...	38.2	1.4	
gi 62988592 qb AC154586.2 	Mus musculus BAC clone RP23-362L12...	38.2	1.4	
gi 62868198 qb AC154363.2 	Mus musculus BAC clone RP23-154K12...	38.2	1.4	
gi 17223145 qb AC097263.6 	Homo sapiens X BAC RP11-298C3 (Ros...	38.2	1.4	
gi 16798968 qb AC099036.1 	Drosophila melanogaster, chromosom...	38.2	1.4	
gi 16648483 qb AY060468.1 	Drosophila melanogaster SD05282 full	38.2	1.4	
gi 53748780 emb CR376826.12 	Zebrafish DNA sequence from clon...	38.2	1.4	

gi 52839510 emb CR293511.11 	Zebrafish DNA sequence from clon...	38.2	1.4
gi 24762667 ref NM_138087.3 	Drosophila melanogaster CG13586-PA	38.2	1.4
gi 15808550 qb AC093289.2 	Homo sapiens chromosome 5 clone RP11-	38.2	1.4

Alignments

Get selected sequences

Select all

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> [gi|4103165|qb|AF021919.1|AF021919](#) Actinobacillus pleuropneumoniae MRP ATPase hor
 RTX protein (apxIVA) genes, complete cds; and beta-galactosidase
 (lacZ) gene, partial cds
 Length=6736


Score = 95.6 bits (48), Expect = 7e-18
 Identities = 48/48 (100%), Gaps = 0/48 (0%)
 Strand=Plus/Plus

```
Query 1      ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAAACAAAATG  48
            |||
Sbjct 594    ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAAACAAAATG  641
```

> [gi|4103979|qb|AF030511.1|AF030511](#) Actinobacillus pleuropneumoniae MRP ATPase hor
 partial cds; ApxIVA var3 (apxIVA) gene, complete cds; and
 beta-galactosidase (lacZ) gene, partial cds
 Length=7004


Score = 87.7 bits (44), Expect = 2e-15
 Identities = 47/48 (97%), Gaps = 0/48 (0%)
 Strand=Plus/Plus

```
Query 1      ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAAACAAAATG  48
            |||
Sbjct 605    ATGAAATGTTAGTGAATTATTTTATTAAATTTGAAAGGAGACAAAATG  652
```

> [gi|18098529|qb|AC093716.3|](#)  Homo sapiens BAC clone RP11-702L4 from 7, complete
 Length=77028

Score = 44.1 bits (22), Expect = 0.022
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Minus


```
Query 18     TATTTTATTAAATTTGAAAGGA  39
            |||
Sbjct 40143  TATTTTATTAAATTTGAAAGGA  40122
```

> [gi|14550318|qb|AC015933.9|](#)  Homo sapiens chromosome 18, clone CTD-2023G8, comp1
 Length=249021

Score = 44.1 bits (22), Expect = 0.022
 Identities = 25/26 (96%), Gaps = 0/26 (0%)
 Strand=Plus/Minus


```
Query 2      TGAAATGTTAGTGAATTATTTTATT  27
```

|||||
Sbjct 42541 TGAAATGTTAGTGAATTATTGTTATT 42516

> [gi|21281558|gb|AC110015.5|](#)  Homo sapiens chromosome 18, clone RP11-104H13, complete
Length=168389


Score = 44.1 bits (22), Expect = 0.022
Identities = 25/26 (96%), Gaps = 0/26 (0%)
Strand=Plus/Minus

Query 2 TGAAATGTTAGTGAATTATTTTATT 27
|||||
Sbjct 102095 TGAAATGTTAGTGAATTATTGTTATT 102070

> [gi|37060013|gb|AC123876.5|](#)  Mus musculus BAC clone RP23-270P19 from chromosome 1
sequence
Length=203639


Score = 42.1 bits (21), Expect = 0.087
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Plus

Query 18 TATTTTATTAATTTGAAAGGAAAC 42
|||||
Sbjct 29103 TATTTTATTAATTTGAAAGGAAAC 29127

> [gi|34740427|gb|AC125373.4|](#)  Mus musculus BAC clone RP23-379A13 from chromosome 1
sequence
Length=190760


Score = 42.1 bits (21), Expect = 0.087
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Minus

Query 18 TATTTTATTAATTTGAAAGGAAAC 42
|||||
Sbjct 6744 TATTTTATTAATTTGAAAGGAAAC 6720

> [gi|37651868|gb|AC125065.3|](#)  Mus musculus BAC clone RP23-430G6 from chromosome 1
sequence
Length=205734


Score = 42.1 bits (21), Expect = 0.087
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

Query 13 TGAATTATTTTATTAATTTG 33
|||||
Sbjct 69284 TGAATTATTTTATTAATTTG 69304

> [gi|25168704|emb|AL845507.8|](#)  Zebrafish DNA sequence from clone CH211-196F15, complete
Length=166074


Score = 42.1 bits (21), Expect = 0.087
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Minus

Query 12 GTGAATTATTTTATTAATTT 32
 |||||
 Sbjct 95258 GTGAATTATTTTATTAATTT 95238

> [gi|31581035|dbj|AP006404.1|](#)  Lotus corniculatus var. japonicus genomic DNA, chi
 clone:LjT43G19, TM0290, complete sequence
 Length=125592


Score = 42.1 bits (21), Expect = 0.087
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 15 AATTATTTTATTAATTTGAA 35
 |||||
 Sbjct 42526 AATTATTTTATTAATTTGAA 42546

> [gi|17149788|gb|AC098861.2|](#)  Homo sapiens BAC clone RP11-297J2 from 4, complete
 Length=185791


Score = 42.1 bits (21), Expect = 0.087
 Identities = 27/29 (93%), Gaps = 0/29 (0%)
 Strand=Plus/Minus

Query 6 ATGTTAGTGAATTATTTTATTAATTTGA 34
 ||||| |
 Sbjct 27117 ATGTTATTAATTATTTTATTAATTTGA 27089

> [gi|25075790|gb|AC007546.6|](#)  Homo sapiens 12 BAC RP11-946P6 (Roswell Park Canc
 Human BAC Library) complete sequence
 Length=168396


Score = 42.1 bits (21), Expect = 0.087
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Minus

Query 28 AATTTGAAAGGAAACAAAATG 48
 |||||
 Sbjct 93168 AATTTGAAAGGAAACAAAATG 93148

> [gi|15808547|gb|AC093214.2|](#)  Homo sapiens chromosome 5 clone CTD-2060C23, comple
 Length=148327

Score = 42.1 bits (21), Expect = 0.087
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 3 GAAATGTTAGTGAATTATTTT 23
 |||||
 Sbjct 141378 GAAATGTTAGTGAATTATTTT 141398

> [gi|15451667|gb|AC016594.7|](#)  Homo sapiens chromosome 5 clone CTD-201003, complete
Length=146235


Score = 42.1 bits (21), Expect = 0.087
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

Query 3 GAAATGTTAGTGAATTATTTT 23
|||||
Sbjct 109754 GAAATGTTAGTGAATTATTTT 109774

> [gi|165657|gb|J03744.1|RABPLP2](#) Rabbit myelin P2 mRNA, complete cds
Length=1836


Score = 42.1 bits (21), Expect = 0.087
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAAGGAAA 41
|||||
Sbjct 1314 TTATTTTATTCATTTGAAAGGAAA 1290

> [gi|28626888|gb|AC129302.3|](#)  Mus musculus BAC clone RP24-441C24 from chromosome
sequence
Length=186647


Score = 40.1 bits (20), Expect = 0.34
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

Query 6 ATGTTAGTGAATTATTTTATTAA 29
|||||
Sbjct 159817 ATGTTAGTGGATTATTTTATTAA 159794

> [gi|38044253|gb|AC102368.6|](#)  Mus musculus chromosome 14, clone RP23-220D8, complete
Length=208781

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 28 AATTTGAAAGGAAACAAAAT 47
|||||
Sbjct 62496 AATTTGAAAGGAAACAAAAT 62515


> [gi|15012100|gb|BC010956.1|](#)  Homo sapiens fibroblast growth factor 7 (keratinocyte growth factor), mRNA (cDNA clone MGC:13629 IMAGE:4282925), complete
cds
Length=1713

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```

Query 15      AATTATTTTATTAAATTGA 34
              |||
Sbjct 1157    AATTATTTTATTAAATTGA 1176

```


> [gi|33235829|gb|AC145772.1|](#)  Pan troglodytes BAC clone RP43-14J20 from 7, complete
Length=165087

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```

Query 17      TTATTTTATTAAATTGAAA 36
              |||
Sbjct 51663   TTATTTTATTAAATTGAAA 51644

```


> [gi|46518131|emb|BX248323.8|](#)  Zebrafish DNA sequence from clone CH211-199J6, complete
Length=177714

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```

Query 15      AATTATTTTATTAAATTGA 34
              |||
Sbjct 50137   AATTATTTTATTAAATTGA 50156

```


> [gi|32402490|gb|AY331807.1|](#)  Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2) gene, complete cds
Length=13180

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```

Query 17      TTATTTTATTAAATTGAAA 36
              |||
Sbjct 11152   TTATTTTATTAAATTGAAA 11133

```


> [gi|4557782|ref|NM_000015.1|](#)  Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA
Length=1276

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```

Query 17      TTATTTTATTAAATTGAAA 36
              |||
Sbjct 1189    TTATTTTATTAAATTGAAA 1170

```

> [gi|70921875|ref|XM_729101.1|](#)  hypothetical protein (PC105701.00.0) mRNA, partial
Length=641

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

```
Query 13      TGAATTATTTTATTAATTT 32
             |||
Sbjct 444      TGAATTATTTTATTAATTT 425
```

> [gi|55630291|ref|XM_519631.1|](#) **G** PREDICTED: Pan troglodytes similar to Arylamine N-acetyltransferase 2 (Arylamide acetylase 2) (Arylamine N-acetyltransferase, polymorphic) (PNAT) (N-acetyltransferase type 2) (NAT-2) (LOC464024), mRNA
 Length=1598

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

```
Query 17      TTATTTTATTAATTTGAAA 36
             |||
Sbjct 1466     TTATTTTATTAATTTGAAA 1447
```

> [gi|70887900|gb|AC151286.3|](#) **B** Mus musculus BAC clone RP23-368B8 from chromosome 1
 sequence
 Length=178835

Score = 40.1 bits (20), Expect = 0.34
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

```
Query 13      TGAATTATTTTATTAATTTGAAA 36
             |||
Sbjct 95904    TGAATTATTTTATTAATTTGAAA 95927
```

> [gi|28227|emb|X14672.1|HSAACT](#) **EG** Human gene for arylamine N-acetyltransferase (H
 Length=1891

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

```
Query 17      TTATTTTATTAATTTGAAA 36
             |||
Sbjct 1803     TTATTTTATTAATTTGAAA 1784
```


> [gi|7630158|emb|AL353012.1|SPBC1711](#) **B** S.pombe chromosome II cosmid c1711
 Length=38000

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

```
Query 17      TTATTTTATTAATTTGAAA 36
             |||
Sbjct 17007    TTATTTTATTAATTTGAAA 17026
```


Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query 17 TTATTTTATTAATTTGAAA 36
 |||||
 Sbjct 17595 TTATTTTATTAATTTGAAA 17614

> [gi|24211331|gb|AC120051.5|](#)  Homo sapiens chromosome 8, clone RP11-809L8, complete
 Length=200827

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus


Query 17 TTATTTTATTAATTTGAAA 36
 |||||
 Sbjct 147211 TTATTTTATTAATTTGAAA 147230

> [gi|41582918|gb|AE017202.1|](#)  Lactobacillus johnsonii NCC 533, section 3 of 7 of
 genome
 Length=305337

Features in this part of subject sequence:
hypothetical protein


Score = 40.1 bits (20), Expect = 0.34
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Minus

Query 9 TTAGTGAATTATTTTATTAATTT 32
 |||||
 Sbjct 39867 TTAGAGAATTATTTTATTAATTT 39844

> [gi|39752574|emb|BX664601.6|](#)  Zebrafish DNA sequence from clone CH211-135J1 in J
 22, complete sequence
 Length=76145

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query 15 AATTATTTTATTAATTTGA 34
 |||||
 Sbjct 14454 AATTATTTTATTAATTTGA 14473


> [gi|38323074|emb|BX465190.4|](#)  Zebrafish DNA sequence from clone DKEY-121A11 in J
 22, complete sequence
 Length=183103

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

```

Query   15      AATTATTTTTTATTAATTTGA   34
          |||||
Sbjct   31944  AATTATTTTTTATTAATTTGA   31925

```


> [gi|28829570|gb|AC117176.2|](#)  Dictyostelium discoideum chromosome 2 map 5018074-
AX4, complete sequence
Length=182871

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```

Query   13      TGAATTATTTTTTATTAATTT   32
          |||||
Sbjct   32116  TGAATTATTTTTTATTAATTT   32097

```


> [gi|58696608|emb|CR356236.12|](#)  Zebrafish DNA sequence from clone CH211-251P4 in
13, complete sequence
Length=171465

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```

Query   15      AATTATTTTTTATTAATTTGA   34
          |||||
Sbjct   51826  AATTATTTTTTATTAATTTGA   51807

```


> [gi|41352298|gb|AY531391.1|](#)  Schizaphis graminum mitochondrion, complete genome
Length=15721

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

```

Query   12      GTGAATTATTTTTTATTAATT   31
          |||||
Sbjct   7453  GTGAATTATTTTTTATTAATT   7434

```


> [gi|27923645|gb|AC137810.3|](#)  Homo sapiens chromosome 5 clone XXfos-102B1, complete
Length=43668

Score = 40.1 bits (20), Expect = 0.34
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Minus

```


Query   9       TTAGTGAATTATTTTTTATTAATTT   32
          |||||
Sbjct   12473  TTAGTGAATTATTTATTATTAATTT   12450

```

> [gi|20198523|gb|AC116333.2|](#)  Homo sapiens chromosome 5 clone CTD-2242E19, complete
Length=112119


Score = 40.1 bits (20), Expect = 0.34
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

Query 9 TTAGTGAATTATTTTATTATTAATTT 32
 |||||
 Sbjct 27260 TTAGTGAATTATTTTATTATTAATTT 27283

> [gi|20197301|gb|AC005171.3|](#)  Arabidopsis thaliana chromosome 2 clone T4E14 map
 sequence
 Length=138181


Score = 40.1 bits (20), Expect = 0.34
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

Query 9 TTAGTGAATTATTTTATTATTAATTT 32
 |||||
 Sbjct 110773 TTAGTAAATTATTTTATTATTAATTT 110796

> [gi|19747134|gb|AC074132.5|](#)  Homo sapiens chromosome 5 clone CTD-2266L18, complete
 sequence
 Length=118131


Score = 40.1 bits (20), Expect = 0.34
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query 4 AAATGTTAGTGAATTATTTTATTATTAATT 31
 |||||
 Sbjct 109572 AAATATTAATGAATTATTTTATTATTAATT 109599

> [gi|19071579|gb|AC025919.8|](#)  Homo sapiens chromosome 15 clone RP11-947024 map 15
 sequence
 Length=188439

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query 15 AATTATTTTATTATTAATTTGA 34
 |||||
 Sbjct 3774 AATTATTTTATTATTAATTTGA 3793


> [gi|15809172|gb|AC093831.3|](#)  Homo sapiens BAC clone RP11-401I19 from 4, complete
 sequence
 Length=182116

Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36
 |||||
 Sbjct 9233 TTATTTTATTATTAATTTGAAA 9214


Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Plus

Query 17 TTATTTTATTATTAATTTGAAA 36
 |||||
 Sbjct 10365 TTATTTTATTATTAATTTGAAA 10384

> [gi|18921296|gb|AC093281.2|](#)  Homo sapiens chromosome 5 clone RP11-414H23, complete
 Length=167455


Score = 40.1 bits (20), Expect = 0.34
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query 4 AAATGTTAGTGAATTATTTTATTAAATT 31
 |||| ||| |||||
 Sbjct 35938 AAATATTAATGAATTATTTTATTAAATT 35965

> [gi|18056697|gb|AC025062.6|](#)  Homo sapiens chromosome 8, clone RP11-685B14, complete
 Length=190459


Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36
 |||||
 Sbjct 190372 TTATTTTATTATTAATTTGAAA 190353

> [gi|45501306|gb|BC067218.1|](#)  Homo sapiens N-acetyltransferase 2 (arylamine N-acetyltransferase)
 mRNA (cDNA clone MGC:71963 IMAGE:4722596), complete cds
 Length=1344


Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36
 |||||
 Sbjct 1186 TTATTTTATTATTAATTTGAAA 1167

> [gi|6457296|gb|AF179626.1|AF179626](#)  Expression vector pGP100, complete sequence
 Length=19012



Score = 40.1 bits (20), Expect = 0.34
 Identities = 20/20 (100%), Gaps = 0/20 (0%)
 Strand=Plus/Minus

Query 17 TTATTTTATTATTAATTTGAAA 36
 |||||
 Sbjct 15283 TTATTTTATTATTAATTTGAAA 15264

>  gi|219415|dbj|D90042.1|HUMAACTA3  Homo sapiens mRNA for arylamine N-acetyltransferase
cds
Length=1276



Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAA 36
|||||
Sbjct 1189 TTATTTTATTAAATTTGAAA 1170

>  gi|219411|dbj|D90040.1|HUMAACTA1  Homo sapiens mRNA for arylamine N-acetyltransferase
cds
Length=1210



Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAA 36
|||||
Sbjct 1123 TTATTTTATTAAATTTGAAA 1104

>  gi|46879303|gb|AC091332.8|  Mus musculus chromosome 17, clone RP23-12K1, complete
Length=216370



Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 13 TGAATTATTTTATTAAATTT 32
|||||
Sbjct 63589 TGAATTATTTTATTAAATTT 63608

>  gi|46309633|gb|AC123880.18|  Mus musculus chromosome 3, clone RP23-225M12, complete
Length=224562

Score = 40.1 bits (20), Expect = 0.34
Identities = 23/24 (95%), Gaps = 0/24 (0%)
Strand=Plus/Plus

Query 17 TTATTTTATTAAATTTGAAAGGAA 40
|||||
Sbjct 166635 TTATTTTATTAAATTTGAAAGGAA 166658

>  gi|2731603|gb|AC003960.1|AC003960  Human Cosmid g5129g129 from 7q31.3, complete
Length=43593

Score = 40.1 bits (20), Expect = 0.34
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 17 TTATTTTATTAAATTTGAAA 36

|||||
 Sbjct 28843 TTATTTTATTAATTTGAAA 28824

> ☐ [gi|24430263|emb|AL928739.5|](#) ☒ Mouse DNA sequence from clone RP23-409L24 on chr10
 sequence
 Length=153028

Score = 40.1 bits (20), Expect = 0.34
 Identities = 23/24 (95%), Gaps = 0/24 (0%)
 Strand=Plus/Plus

Query 6 ATGTTAGTGAATTATTTTATTAA 29
 |||||
 Sbjct 72495 ATGTTAGTGGATTATTTTATTAA 72518

Get selected sequences

Select all

Deselect all

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Aug 9, 2005 12:07 AM

Number of letters in database: 2,000,247,405

Number of sequences in database: 3,413,089

Lambda K H
 1.37 0.711 1.31

Gapped
 Lambda K H
 1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 3413089

Number of Hits to DB: 3386291

Number of extensions: 280204

Number of successful extensions: 93444

Number of sequences better than 10: 123

Number of HSP's better than 10 without gapping: 123

Number of HSP's gapped: 93444

Number of HSP's successfully gapped: 124

Number of extra gapped extensions for HSPs above 10: 92053

Length of query: 48

Length of database: 14885149293

Length adjustment: 20

Effective length of query: 28

Effective length of database: 14816887513

Effective search space: 414872850364

Effective search space used: 414872850364

A: 0

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 12 (24.3 bits)

S2: 18 (36.2 bits)



results of BLAST

BLASTN 2.2.11 [Jun-05-2005]

Query:

Database: nr

#	Fields:	Query id,	Subject id,	% identity,	alignment length,	mismatches,	gap openin
1_24169	gi 4103165 gb AF021919.1 AF021919	100.00	4004	0	0	2733	
1_24169	gi 4103165 gb AF021919.1 AF021919	100.00	2677	0	0	1	
1_24169	gi 4103979 gb AF030511.1 AF030511	97.94	2722	52	4	2733	
1_24169	gi 4103979 gb AF030511.1 AF030511	97.09	1442	34	8	5299	
1_24169	gi 4103979 gb AF030511.1 AF030511	99.14	1277	11	0	1401	
1_24169	gi 4103979 gb AF030511.1 AF030511	87.57	1360	98	58	1	
1_24169	gi 6671147 gb AF188867.1 AF188867	100.00	391	0	0	6044	
1_24169	gi 6671147 gb AF188867.1 AF188867	98.72	234	3	0	5219	
1_24169	gi 6671147 gb AF188867.1 AF188867	97.35	151	4	0	4864	
1_24169	gi 6671147 gb AF188867.1 AF188867	96.69	151	5	0	5689	
1_24169	gi 6671147 gb AF188867.1 AF188867	91.67	156	9	4	4474	
1_24169	gi 6671145 gb AF188866.1 AF188866	100.00	391	0	0	6044	
1_24169	gi 6671145 gb AF188866.1 AF188866	98.72	234	3	0	5219	
1_24169	gi 6671145 gb AF188866.1 AF188866	97.35	151	4	0	4864	
1_24169	gi 6671145 gb AF188866.1 AF188866	96.69	151	5	0	5689	
1_24169	gi 6671145 gb AF188866.1 AF188866	91.67	156	9	4	4474	
1_24169	gi 6671143 gb AF188865.1 AF188865	100.00	391	0	0	6044	
1_24169	gi 6671143 gb AF188865.1 AF188865	98.72	234	3	0	5219	
1_24169	gi 6671143 gb AF188865.1 AF188865	97.35	151	4	0	4864	
1_24169	gi 6671143 gb AF188865.1 AF188865	96.69	151	5	0	5689	
1_24169	gi 6671143 gb AF188865.1 AF188865	91.67	156	9	4	4474	
1_24169	gi 6671141 gb AF188864.1 AF188864	100.00	391	0	0	6044	
1_24169	gi 6671141 gb AF188864.1 AF188864	98.72	234	3	0	5219	
1_24169	gi 6671141 gb AF188864.1 AF188864	97.35	151	4	0	4864	
1_24169	gi 6671141 gb AF188864.1 AF188864	96.69	151	5	0	5689	
1_24169	gi 6671141 gb AF188864.1 AF188864	91.67	156	9	4	4474	
1_24169	gi 6671139 gb AF188863.1 AF188863	100.00	391	0	0	6044	
1_24169	gi 6671139 gb AF188863.1 AF188863	98.72	234	3	0	5219	
1_24169	gi 6671139 gb AF188863.1 AF188863	97.35	151	4	0	4864	
1_24169	gi 6671139 gb AF188863.1 AF188863	96.69	151	5	0	5689	
1_24169	gi 6671139 gb AF188863.1 AF188863	91.67	156	9	4	4474	
1_24169	gi 6671137 gb AF188862.1 AF188862	100.00	391	0	0	6044	
1_24169	gi 6671137 gb AF188862.1 AF188862	98.72	234	3	0	5219	
1_24169	gi 6671137 gb AF188862.1 AF188862	97.35	151	4	0	4864	
1_24169	gi 6671137 gb AF188862.1 AF188862	96.69	151	5	0	5689	
1_24169	gi 6671137 gb AF188862.1 AF188862	91.67	156	9	4	4474	
1_24169	gi 6671135 gb AF188861.1 AF188861	100.00	391	0	0	6044	
1_24169	gi 6671135 gb AF188861.1 AF188861	98.72	234	3	0	5219	
1_24169	gi 6671135 gb AF188861.1 AF188861	97.35	151	4	0	4864	
1_24169	gi 6671135 gb AF188861.1 AF188861	96.69	151	5	0	5689	
1_24169	gi 6671135 gb AF188861.1 AF188861	91.67	156	9	4	4474	
1_24169	gi 6671133 gb AF188860.1 AF188860	100.00	391	0	0	6044	
1_24169	gi 6671133 gb AF188860.1 AF188860	98.72	234	3	0	5219	
1_24169	gi 6671133 gb AF188860.1 AF188860	97.35	151	4	0	4864	
1_24169	gi 6671133 gb AF188860.1 AF188860	96.69	151	5	0	5689	
1_24169	gi 6671133 gb AF188860.1 AF188860	91.67	156	9	4	4474	
1_24169	gi 6671129 gb AF188858.1 AF188858	100.00	391	0	0	6044	
1_24169	gi 6671129 gb AF188858.1 AF188858	98.72	234	3	0	5219	
1_24169	gi 6671129 gb AF188858.1 AF188858	97.35	151	4	0	4864	
1_24169	gi 6671129 gb AF188858.1 AF188858	96.69	151	5	0	5689	
1_24169	gi 6671129 gb AF188858.1 AF188858	91.67	156	9	4	4474	
1_24169	gi 6671127 gb AF188857.1 AF188857	100.00	391	0	0	6044	

1_24169	gi 6671127 gb AF188857.1 AF188857	98.72	234	3	0	5219
1_24169	gi 6671127 gb AF188857.1 AF188857	97.35	151	4	0	4864
1_24169	gi 6671127 gb AF188857.1 AF188857	96.69	151	5	0	5689
1_24169	gi 6671127 gb AF188857.1 AF188857	91.67	156	9	4	4474
1_24169	gi 6671131 gb AF188859.1 AF188859	96.94	392	10	2	6044
1_24169	gi 6671131 gb AF188859.1 AF188859	93.62	235	13	2	5219
1_24169	gi 6671131 gb AF188859.1 AF188859	91.19	159	12	2	4470
1_24169	gi 6671131 gb AF188859.1 AF188859	93.57	140	7	2	4876
1_24169	gi 6671131 gb AF188859.1 AF188859	92.86	140	8	2	5701
1_24169	gi 6671151 gb AF188869.1 AF188869	92.60	392	27	2	6044
1_24169	gi 6671151 gb AF188869.1 AF188869	89.04	228	23	2	5219
1_24169	gi 6671149 gb AF188868.1 AF188868	92.35	392	28	2	6044
1_24169	gi 6671149 gb AF188868.1 AF188868	89.04	228	23	2	5219
1_24169	gi 1655856 gb U62625.1 APU62625 99.16	119	0	1	6619	6736